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HY-10-12	KEERPPPPRVVHPLIGLCEYGGSDYEEEEEQTPPPPPPTAQ'QKREEQTKKENEDKLTWDNKLACLLCRRQFPNKEVL 970
LOC15	PEJVRNGDEENPLKRGVAAVYSGSDHEE.....ELVERLESEEEKLADHKKMACLLCRRQFPNKDAL 662
DXS8237E	DLPELASDURFPPRGLVAAVYSGSDSEE.....EQERGGPEREEKLTDWQKLACLLCRRQFPNKEAL 233
HY-10-12	TEHQQLSDLPKQHLETHRRKTKQSQELAYLERRERE.GKFKCRGNDRREKLQSFDSPEKRIKYSRETDS..DRKLVDKEDID 1050
LOC15	VRIHQQLSDLIKQNHDIYRRSRHSEQHEALELKRERE.MKYRDRAAERREKYGIPEPPEPKRKKQFDAGTV..NYEQPTKDGID 742
DXS8237E	TEHQQLSGLHKQHLETHRRRAHLSHHFLEALELKNHMEQMKYRDRAAERREKYGIPEPPEPKRKYGGJSTASVDFEQPTKGLC 316
HY-10-12	TSISGGLVLAQATGWRKGTGLGYHLPGLASSFEAEGRMRGSPVGAUGIKTSKRQSNETYRDVRRVNFARYKELD 1123
LOC15	HENIGNKMLQAMGWREGSGLGRKKQCTTAFIEAQVRLKGAGLGAAGSAYGLSGADSYKDAVRKAMFARFEME 815
DXS8237E	SINIGSRHJQAMGWKEGSGLGRKKQGIPTPIEAQTRVRGSGLGARGSSYGVSTESYKETLHKTWVTRFNEAQ 389

Figure 1

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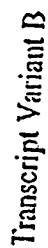
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Figure 2

[illegible]

Fig 2 (contd)

Fig 2 (cont'd)



AAGGAGGACGGCGCTGGAGCCTTCGCCGCTAGGTACTGCCTATACCAGAAATTGGTATTAACAAGNTTTACTTETISGGCCCTCTTGATAAAGAAGATCTGGGGGNTTCTCGAC 120 (12D)

CTGCTAACACAACTGGACCTTTCTCA

197 M A E K R V G R A G I G L I T S S D F P T S A S Q S A G T I C

EIGASGCAAGGACCGICCATIIGATITGAACGGAGANTILALIAHUAUUGAGAGAGGTICTACATCAUGTCTBAAGCTIRRGAGTTCMAIGAMNATTIAGJGGGAPC 260 (14S)

V S H R T C H L D N Q S A E F Y Y L H A T D V I J H C S E A W S S H E K F S G S

CANGAGNAGAGGTTTCTUCGGGTGG...  
Q E E R F A P G K..

Fig. 3a

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Figure 3b.

227bp exon:

GACTGGGTGAAAGCTTTTCTGCAGCAGTCATGTTAAAAACCTTGTGTTGACTTTCTCTCG  
TGTCTGAAACTAAC  
AGAACTGGACCTTTTCGGACTGGGTGAAAGCTTTTCTGCAGCAGTCATGTTGAAAACC  
TTGTGTTGACTTTCTT  
CGTGTCTGAAATGGGAGCATAAAAGTTACTCCGCCACTTCGTCTTAAATAGCAAAAC  
TTTGCTGTTTCTGCAG

137bp exon:

ATCTAGGACCTTGTACAGAACTCTGCCAAAAAATGTTTACAGAAGAATGTGCTGT  
GATTAGAGAAGAATA  
TGCTGGTGTGTAGATTTCAAACCTCTCTGGACAATATGAATAACACTGTCTTTGTTTCTAC  
AG

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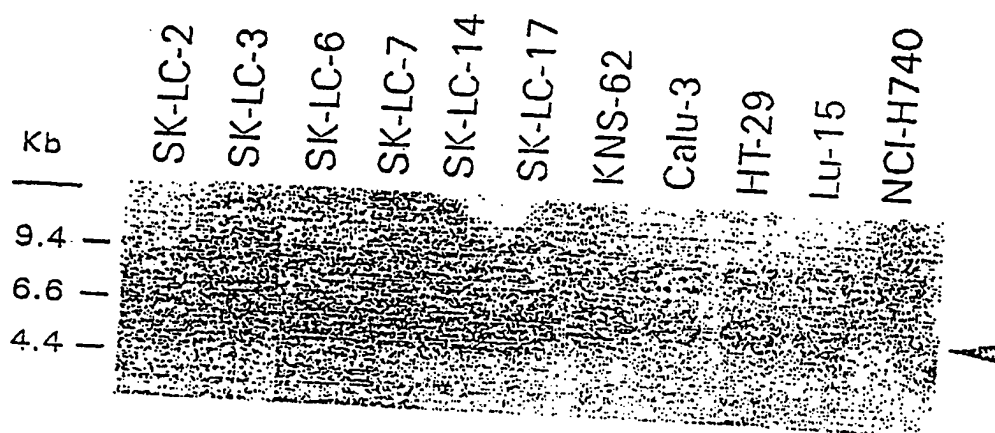


Figure 4

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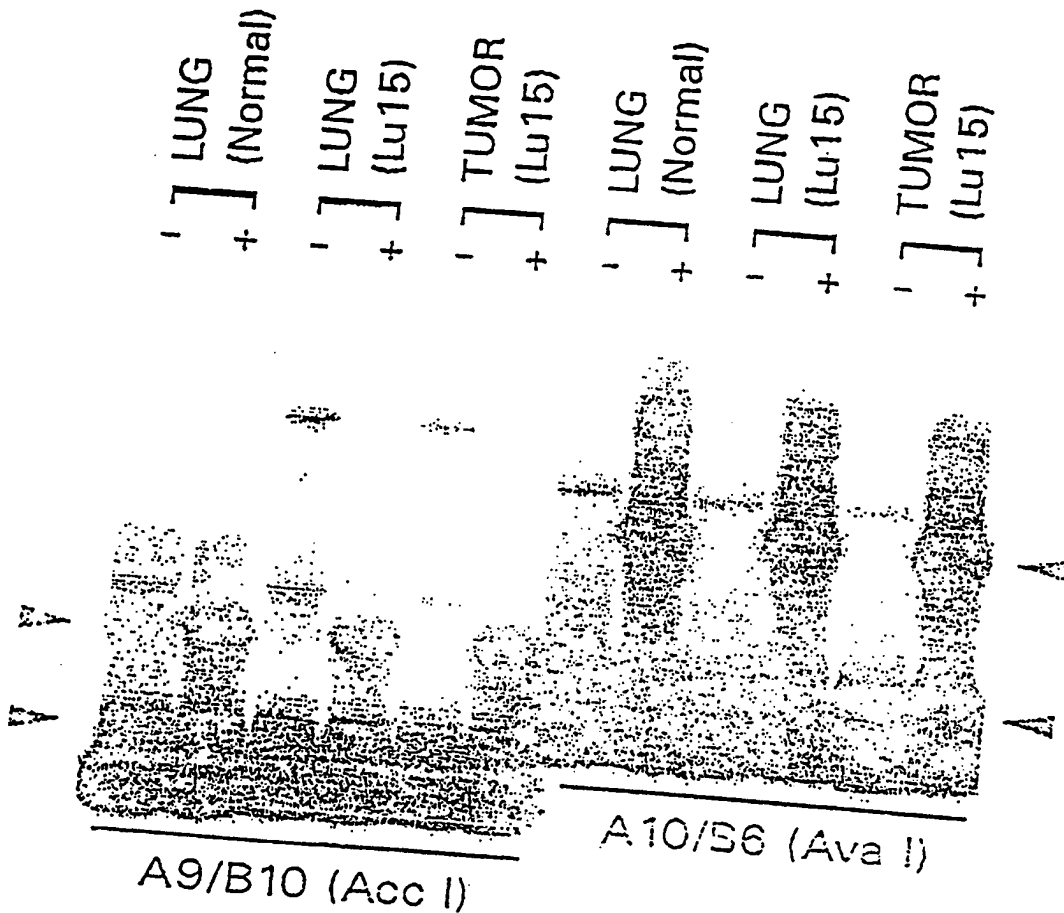


Figure 5